

**AMENDMENTS TO THE DRAWINGS:**

Replacement drawing sheets showing amended Figures 1, 3, 9D, 10A and 10D, without markings, is attached herewith on a separate sheet in compliance with §1.84(p)(5).

Annotated drawing sheets showing amended Figures 1, 3, 9D, 10A and 10D, with markings, is attached herewith on a separate sheet in compliance with §1.84(p)(5).

**REMARKS**

Entry of the foregoing, and early and favorable consideration of the subject application on the merits are respectfully requested.

By the present Amendment, the specification has been amended to incorporate a revised sequence listing, and to insert SEQ ID numbers into the specification and claims. Claim 37 is amended to clarify that the DNA encodes a polypeptide. No new matter has been added.

In the event that there are any questions concerning this Amendment, or the application in general, the Examiner is respectfully urged to telephone Applicants' undersigned representative, so that prosecution of the application may be expedited.

Respectfully submitted,

BUCHANAN INGERSOLL PC  
(INCLUDING THE ATTORNEYS FROM BURNS DOANE SWECKER & MATHIS)

Date: December 7, 2005

By: 

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Enclosures: Five (5) sheets of Replacement drawings (FIGS. 1, 3, 9D, 10A and 10D)  
Five (5) sheets of Annotated drawings showing changes (FIGS. 1, 3, 9D, 10A and 10D)

ANNOTATED SHEET SHOWING CHANGES

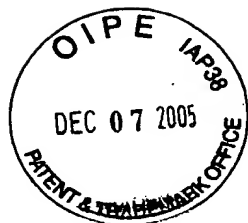
Application No. 09/900,963

Attorney Docket No.: 010830-118

Inventor(s): Claudine Guerin-Marchand et al.

PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P. FALCIPARUM  
BEARING EPITOPE CAPABLE OF STIMULATING THE T LYMPHOCYTES

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(5') 1 SDLEQERRAKEKLQEQQ  
18 SDLEQDRLAKEKLQEQQ  
35 SDLEQERLAKEKLQEQQ  
52 SDLEQERRAKEKLQEQQ  
69 SDLEQERRAKEKLQEQQ  
86 SDLEQDRLAKEKLQEQQ  
103 SDLEQERRAKEKLQEQQ  
120 SDLEQERRAKEKLQEQQ  
137 SDLEQERLAKEKLQEQQ  
154 SDLEQERRAKEKLQEQQ  
171 SDLEQERRAKEKLQEQQ  
188 SDLEQERRAKEKLQEQQ  
205 RDLEQ

R

210 RKADTKKNLERKKKEHGDILAEDLYGRLEIP  
240 AIELPSENERGYYPHQSSLPQDNRGNSRD  
270 SKEISIIIEKTNRESITTNVEGRRDIHKGHL  
300 EEKKGSIKPEQKEDKS 316 (3')

**FIGURE 1**

ANNOTATED SHEET SHOWING CHANGES

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RDELFNELLNSVDVNGEVKENILEESQVND<sup>E</sup>~~V~~IFNSLVJSVQQEQQ  
HNVEEKVEESVEENDEESVEENVEENVEENDDGSVASSVEESI  
ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE  
ESVAPSVEESVAEMLKER

**FIGURE 3**

ANNOTATED SHEET SHOWING CHANGES

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1261 / 421	1291 / 431	
AAA GGA AAG AAA TAT GAA AAA ACA AAG GAT AAT AAT TTT AAA CCA AAT GAT AAA AGT TTG		
lys gly lys lys tyr glu lys thr lys asp asn phe lys pro asn asp lys ser leu		
1321 / 441	1351 / 451	
TAT GAT GAG CAT ATT AAA AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA		
tyr asp glu his ile lys lys tyr lys asn asp lys gln val asn lys glu lys glu lys		
1381 / 461	1411 / 471	
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA AAT GAA ATT TTA CAG ATC GIG GAT		
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp		
1441 / 481	1471 / 491	
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT		
glu leu ser glu asp ile thr lys tyr phe met lys leu <del>0GH lys val ile tyr</del>		

FIGURE 9D

# ANNOTATED SHEET SHOWING CHANGES

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LSN.3'STOP -> 1-phase Translation

DNA sequence 1482 b.p. CAAGAACAACAA ... ATGAAACTATAA linear

1 / 1 31 / 11  
CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA GAA  
gln glu gln gln ser asp leu glu gln gln arg ala lys glu lys leu gln glu gln  
61 / 21 91 / 31  
CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT  
gln ser asp leu glu gln gln asp arg leu ala lys glu lys leu gln glu gln gln ser asp  
121 / 41 151 / 51  
TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT CTA GAA CAA  
leu glu gln glu arg leu ala lys glu lys leu gln glu gln gln ser asp leu glu gln  
181 / 61 211 / 71  
GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT  
glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu arg arg  
241 / 81 271 / 91  
GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA  
ala lys glu lys leu gln glu gln gln ser asp leu glu gln asp arg leu ala lys glu  
301 / 101 331 / 111  
AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA  
lys leu gln glu gln gln ser asp leu glu gln glu arg ala lys glu lys leu gln

FIGURE 10A



1321 / 441	1351 / 451	
TAT GAT GAG CAT ATT AAA AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA		
tyr asp glu his ile lys lys tyr lys asn asp lys gln val asn lys glu lys glu lys		
1381 / 461	1411 / 471	
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT		
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp		
1441 / 481	1471 / 491	
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT		
glu leu ser glu asp ile thr lys tyr phe met lys leu <del>GGT lys val ile tyr</del>		

**FIGURE 10D**